

Fig. 1

<i>Gene</i>	x-fold stronger in the atrium MW n =6	Genbank Acc. No.
Sarcolipin	9.6	NM_003063
myosin. light polypeptide 4. alkali; atrial. embryonic	9.2	M36172
A kinase (PRKA) anchor protein 3	8.7	NM_006422
potassium channel. subfamily K. member 1 (TWIK-1)	6.7	U90065
up-regulated by BCG-CWS	5.6	AB040120
myosin. heavy polypeptide 6. cardiac muscle. alpha (cardiomyopathy. hypertrophic 1)	5.3	D00943
titin immunoglobulin domain protein (myotilin)	5.2	NM_006790
signal transducer and activator of transcription 4	4.9	NM_003151
nuclear receptor subfamily 2. group F. member 1 (COUP-TF 1)	4.2	AI951185
NADP-dependent retinol dehydrogenase/reductase	4.2	NM_005771
natriuretic peptide precursor B	4.2	NM_002521
desmocollin 1	4.1	NM_004948
potassium voltage-gated channel. shaker-related subfamily. member 5 (KCNA5)	4.0	NM_002234
secreted frizzled-related protein 1	4.0	NM_003012
phospholipase A2. group IIA (platelets. synovial fluid)	3.8	NM_000300
keratin 18	3.7	NM_000224

<i>Gene</i>	x-fold stronger in the atrium MW n =6	Genbank Acc. No.
dickkopf homolog 3 (Xenopus laevis)	3.7	NM_013253
natriuretic peptide precursor A	3.5	M30262
guanine nucleotide binding protein (G protein). beta 5	3.4	NM_006578
potassium channel. subfamily K. member 3 (TASK-1)	3.3	NM_002246
H factor 1 (complement)	3.1	X04697
up-regulated by BCG-CWS	3.0	NM_022154
Phosphodiesterase 8B	3.0	AK023913
cartilage oligomeric matrix protein (pseudoachondroplasia. epiphyseal dysplasia 1. multiple)	2.9	NM_000095
complement component 3	2.7	NM_000064
sparc/osteonectin. cwcv and kazal-like domains proteoglycan (testican)	2.7	AF231124
phospholipase C. beta 1 (phosphoinositide-specific)	2.7	AL049593
actin. alpha 2: smooth muscle. aorta	2.7	NM_001613
chromosome 1 open reading frame 15	2.6	AF288395
corin	2.6	NM_006587
myosin light chain 2a	2.5	NM_021223
transmembrane 6 superfamily member 1	2.4	NM_023003
FK506 binding protein 11. 19 kDa	2.4	NM_016594
visinin-like 1	2.4	NM_003385

<i>Gene</i>	x-fold stronger in the atrium MW n =6	Genbank Acc. No.
angiotensin II receptor. type 1	2.4	NM_004835
H factor (complement)-like 2	2.3	X56210
NY-REN-58 antigen	2.3	NM_016122
similar to neuralin 1	2.2	AL049176
Duffy blood group	2.1	NM_002036
transgelin	2.0	NM_003186
potassium intermediate/small conductance calcium- activated channel. subfamily N. member 2	2.0	NM_021614
endothelin receptor type A	2.0	NM_001957
spermidine/spermine N1-acetyltransferase	2.0	NM_002970
transmembrane 4 superfamily member 2	2.0	NM_004615
B-cell translocation gene 1. anti-proliferative	2.0	NM_001731
phospholipase A2-group V	1.9	AL158172
fibulin 1	1.9	Z95331
spermidine/spermine N1-acetyltransferase	1.9	M55580
peptidylglycine alpha-amidating monooxygenase	1.9	BF038548
spermidine/spermine N1-acetyltransferase	1.9	BE971383
hephaestin	1.9	NM_014799
Ras-related associated with diabetes	1.9	NM_004165
growth hormone receptor	1.8	NM_000163

<i>Gene</i>	x-fold stronger in the atrium MW n =6	Genbank Acc. No.
peptidylglycine alpha-amidating monooxygenase	1.8	NM_000919
WNT1 inducible signaling pathway protein 2	1.8	NM_003881
melanophilin	1.8	NM_024101
B-cell translocation gene 1. anti-proliferative	1.8	AL535380
adipose specific 2	1.8	NM_006829
reticulon 4	1.8	AF333336
protein kinase. AMP-activated. gamma 2 non-catalytic subunit	1.8	NM_016203
proteolipid protein 2 (colonic epithelium-enriched)	1.8	NM_002668
CD44 antigen (homing function and Indian blood group system)	1.8	BE903880
T-box 5	1.8	NM_000192
actinin. alpha 1	1.7	AI082078
D123 gene product	1.7	NM_006023
Ris	1.7	NM_016563
complement component 1. r subcomponent	1.7	AL573058
peroxiredoxin 1	1.7	L19184
S100 calcium binding protein A4 (calcium protein. calvasculin. metastasin. murine placental homolog)	1.6	NM_002961
annexin A4	1.6	NM_001153

<i>Gene</i>	x-fold stronger in the atrium MW n =6	Genbank Acc. No.
phospholipase A2. group V	1.6	NM_000929
tubulin. beta polypeptide	1.6	NM_001069
prostaglandin I2 (prostacyclin) synthase	1.6	NM_000961
Homo sapiens clone 24416 mRNA sequence	1.6	AV712602
complement component 7	1.6	NM_000587
epidermal growth factor receptor pathway substrate 8	1.6	NM_004447
aldo-keto reductase family 1. member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase. type III)	1.6	M33376
C1q and tumor necrosis factor related protein 1	1.6	NM_030968
reticulon 4	1.5	AB015639
CD47 antigen (Rh-related antigen. integrin-associated signal transducer)	1.5	BG230614
hypothetical protein FLJ10097	1.5	AF523320
peptidylglycine alpha-amidating monooxygenase	1.5	AI022882
glutathione peroxidase 3 (plasma)	1.5	AW149846
catenin (cadherin-associated protein). alpha-like 1	1.5	NM_003798
DKFZP586A0522 protein	1.5	NM_014033
integrin associated protein mRNA	1.5	Z25521
homolog of yeast long chain polyunsaturated fatty acid elongation enzyme 2	1.5	AL136939

<i>Gene</i>	x-fold stronger in the atrium MW n =6	Genbank Acc. No.
reticulon 4	1.5	AF320999
annexin A1	1.5	NM_000700
HIV-1 TAR RNA binding protein (TARBP-b)	1.5	L22453
DEK oncogene (DNA binding)	1.5	NM_003472
CCAAT/enhancer binding protein (C/EBP). delta	1.5	NM_005195
aldo-keto reductase family 1. member A1 (aldehyde reductase)	1.5	NM_006066
KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	1.4	NM_006854
tropomyosin 1 (alpha)	1.4	Z24727
hydroxysteroid (17-beta) dehydrogenase 12	1.4	NM_016142
tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy. pseudoinflammatory)	1.4	NM_000362
ADP-ribosylation-factor-like 5	1.4	NM_012097
nucleosome assembly protein 1-like 1	1.4	NM_004537
peptidylprolyl isomerase B (cyclophilin B)	1.4	NM_000942
delta-like 1 homolog (Drosophila)	0.1	U15979
myosin. light polypeptide 3. alkali; ventricular. skeletal. slow	0.1	NM_000258

<i>Gene</i>	x-fold stronger in the atrium MW n =6	Genbank Acc. No.
HSKM-B protein	0.1	AF070592
ankyrin repeat domain 2 (stretch responsive muscle)	0.2	NM_020349
KIAA1733 protein	0.2	AW054711
four and a half LIM domains 2	0.2	NM_001450
carboxypeptidase. vitellogenic-like	0.3	NM_031311
protein tyrosine phosphatase. non-receptor type 3	0.3	NM_002829
myosin. light polypeptide 2. regulatory. cardiac. slow	0.3	AF020768
gamma-aminobutyric acid (GABA) A receptor. alpha 4	0.3	NM_000809
dihydropyrimidinase-like 4	0.3	NM_006426
hypothetical protein FLJ20156	0.4	NM_017691
hypothetical protein FLJ14054	0.4	NM_024563
potassium inwardly-rectifying channel. subfamily J. member 2	0.4	AF153820
hypothetical protein FLJ32389	0.4	AL551046
ribosomal protein L3-like	0.4	NM_005061
NDRG family member 4	0.4	AV724216
hairy/enhancer-of-split related with YRPW motif 2	0.4	NM_012259
Homo sapiens. clone MGC:8772 IMAGE:3862861. mRNA. complete cds	0.4	BG332462
isocitrate dehydrogenase 2 (NADP+). mitochondrial	0.4	U52144

<i>Gene</i>	x-fold stronger in the atrium MW n =6	Genbank Acc. No.
likely ortholog of mouse limb-bud and heart gene	0.5	NM_030915
hypothetical protein FLJ21901	0.5	NM_024622
phospholipase C-like 1	0.5	NM_006226
lipoprotein lipase	0.5	NM_000237
LRP16 protein	0.5	NM_014067
phosphofructokinase. muscle	0.5	U24183
LIM domain binding 3	0.5	AA211481
protein kinase (cAMP-dependent. catalytic) inhibitor alpha	0.6	NM_006823
potassium inwardly-rectifying channel. subfamily J. member 8	0.6	BF514158
H2B histone family. member Q	0.6	NM_003528
NS1-binding protein	0.6	AF205218
acetyl-Coenzyme A acetyltransferase 1 (acetoacetyl Coenzyme A thiolase)	0.6	NM_000019
hyaluronoglucosaminidase 1	0.6	AF173154
potassium inwardly-rectifying channel. subfamily J. member 4	0.6	NM_004981
ras-like protein TC10	0.6	BF348067
crystallin. mu	0.6	NM_001888
ubiquitin specific protease 13 (isopeptidase T-3)	0.6	NM_003940

<i>Gene</i>	x-fold stronger in the atrium MW n =6	Genbank Acc. No.
ras-like protein TC10	0.7	BF348067
actin. alpha 1. skeletal muscle	0.7	NM_001100
L-3-hydroxyacyl-Coenzyme A dehydrogenase. short chain	0.7	AF001903
heat shock 27kDa protein family. member 7 (cardiovascular)	0.7	NM_014424

Fig. 2:

Gene	Genbank Accession Number	Sequence of primer 1 5'-3'	Sequence of primer 2 5'-3'	Sequence of probe 5'-3'
TWIK-1	NM_002245 SEQ ID NO:1	tgaagaaggacaaggacgagga SEQ ID NO:2	gcctggctgtgatcgagga SEQ ID NO:3	caggtgcacatcatagagcatgaccaa SEQ ID NO:4
TASK-1	AF065163 SEQ ID NO:5	acgtctacgcggaggtgct SEQ ID NO:6	tctcgcggtcttgtacc SEQ ID NO:7	cacttcagtcctatgtctcgtgcct SEQ ID NO:8
GIRK1	NM_002239 SEQ ID NO:9	gtccacgcaacattgaag SEQ ID NO:10	gggacgacatgagaagcatt SEQ ID NO:11	cccacccaccttacagtgtgaaa SEQ ID NO:12
SK2	AF239613 SEQ ID NO:13	tgacagccctggtgtag SEQ ID NO:14	tccatcatgaaattgtgcacg SEQ ID NO:15	tggcaagggaagctagaacttacc SEQ ID NO:16
PCN1	NM_002234 SEQ ID NO:17	cagggaacccatttcttagcat SEQ ID NO:18	tgtccccgtagcccacagt SEQ ID NO:19	acgccttctggtgggcagtggtc SEQ ID NO:20
beta-Actin	NM_001101 SEQ ID NO:21	tccaccttcagcagatgtg SEQ ID NO:22	ctagaagcatttgcggtggac SEQ ID NO:23	atcagcaagcaggagtatgacggtccg SEQ ID NO:24

Fig. 3

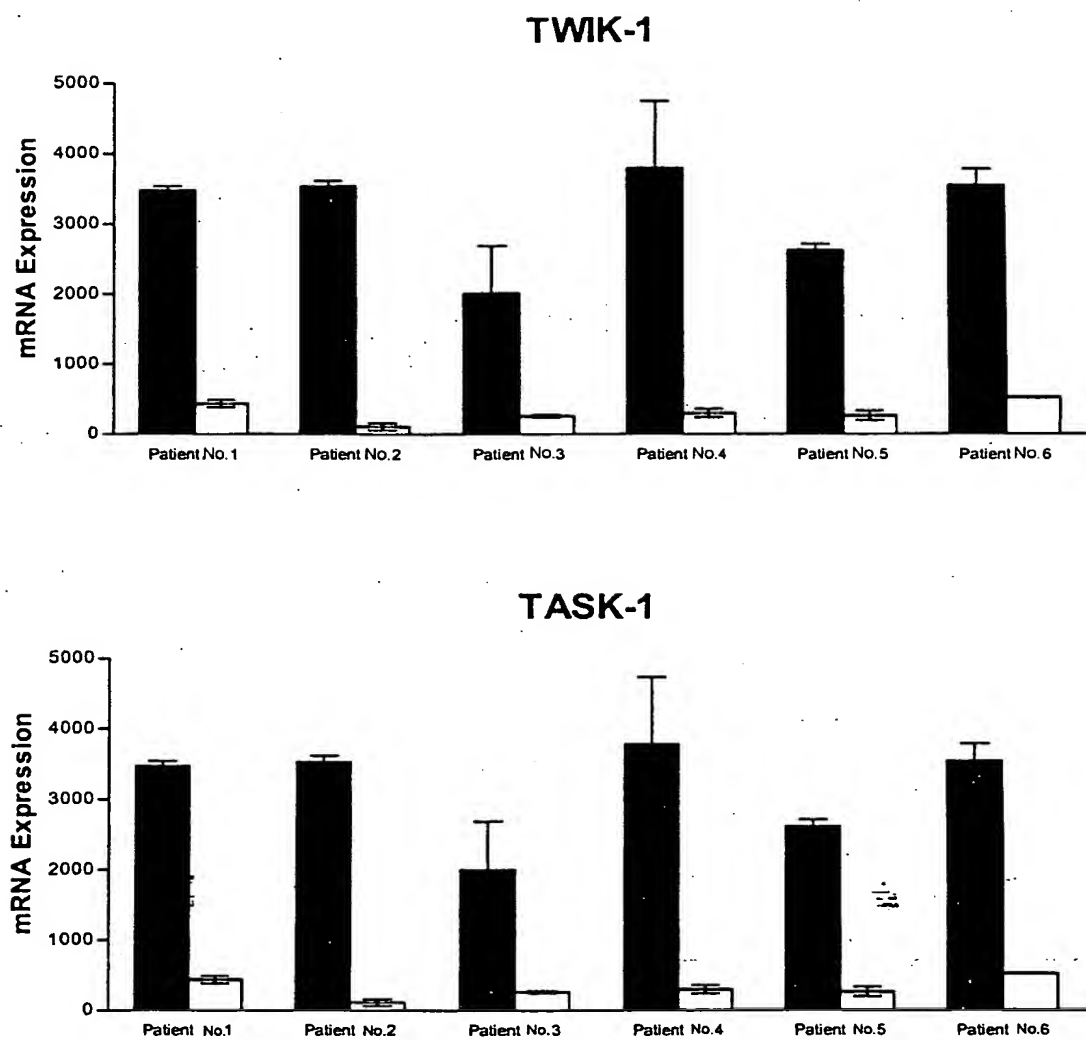


Fig. 3, Continued

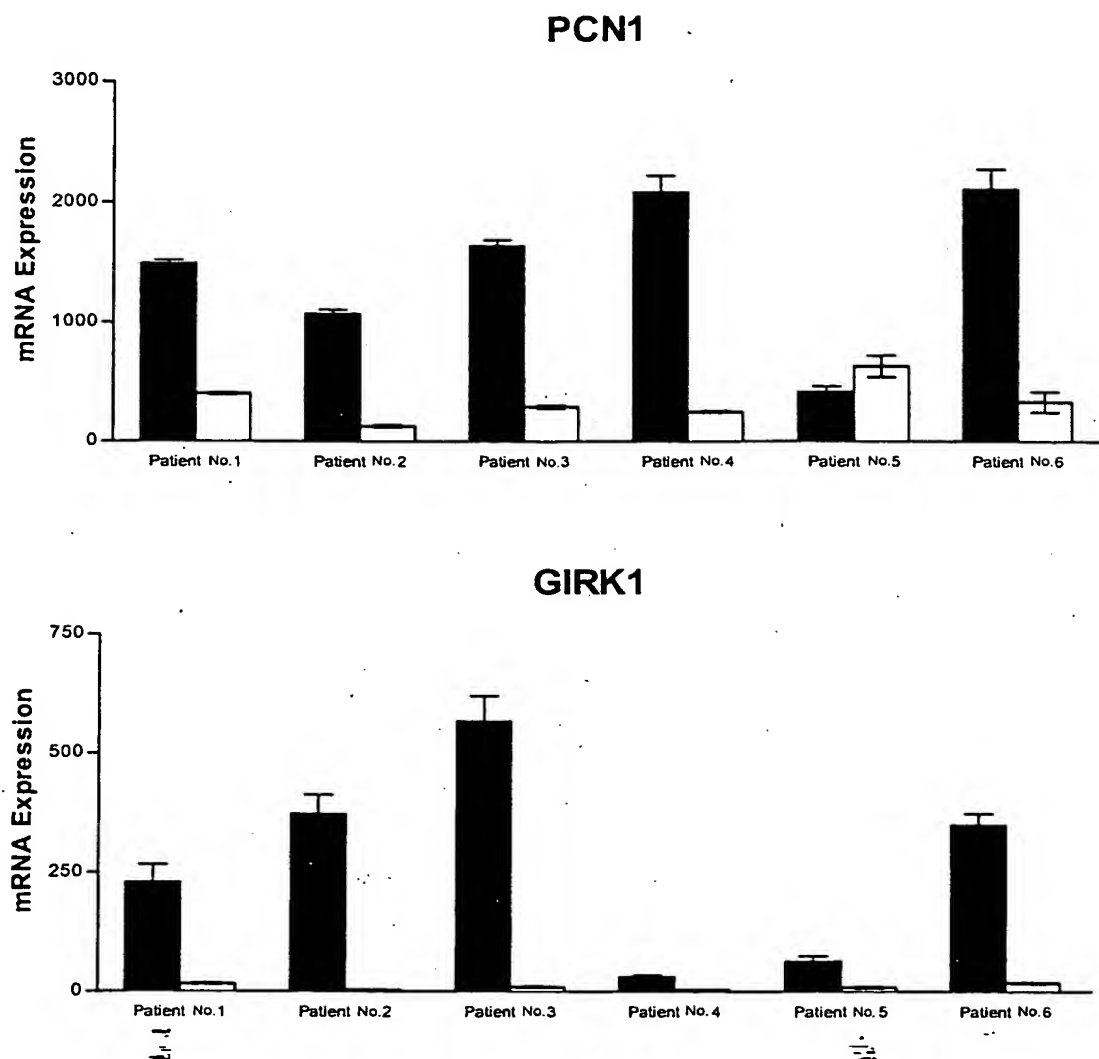


Fig. 3, Continued

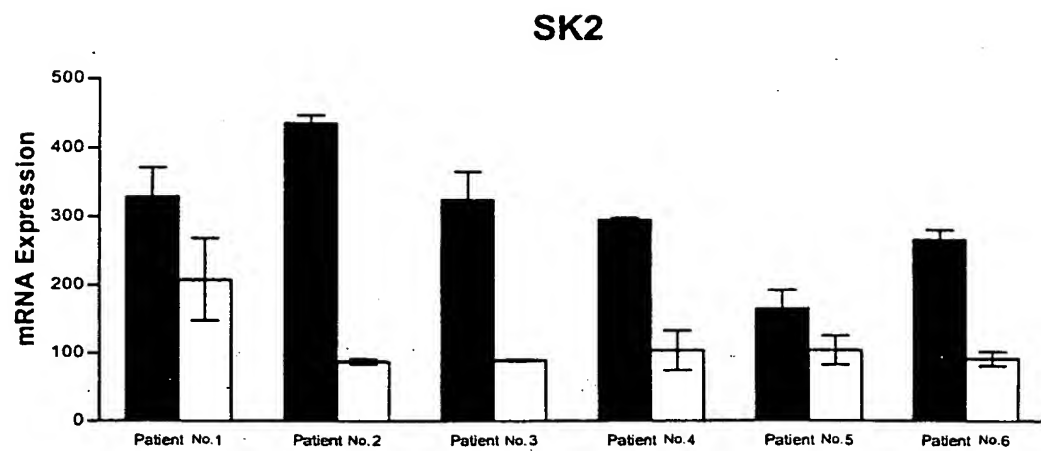


Fig. 4

